

1652

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/456,306

DATE: 02/26/2001  
TIME: 10:32:18

Input Set : A:\ES.txt  
Output Set: N:\CRF3\02262001\I456306.raw

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3 <110> APPLICANT: Degussa-Hols AG  
5 <120> TITLE OF INVENTION: Novel nucleotide sequences coding for the poxB gene  
7 <130> FILE REFERENCE: 990159 BT  
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/456,306  
C--> 10 <141> CURRENT FILING DATE: 1999-12-08  
12 <160> NUMBER OF SEQ ID NOS: 3  
14 <170> SOFTWARE: PatentIn Ver. 2.1  
16 <210> SEQ ID NO: 1  
17 <211> LENGTH: 2160  
18 <212> TYPE: DNA  
19 <213> ORGANISM: Corynebacterium glutamicum  
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36 cgaggcgacc agacaggcgt gcccacgatg tttaaataagg cgatcggtgg gcatctgtgt 120  
38 ttggtttcga cgggctgaaa ccaaaccaga ctgcccagca acgacggaaa tcccaaaaagt 180  
40 gggcatccct gtttggtagc gactaccac ccgggcctga aactccctgg caggcgggcg 240  
42 aagcgtggca acaactggaa tttaagagca caattgaagt cgcaccaagt taggcaaac 300  
44 aatagccata acgttgagga gttcag atg gca cac agc tac gca gaa caa tta 353  
45 Met Ala His Ser Tyr Ala Glu Gln Leu  
46 1 5  
48 att gac act ttg gaa gct caa ggt gtg aag cga att tat ggt ttg gtg 401  
49 Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile Tyr Gly Leu Val  
50 10 15 20 25  
52 ggt gac agc ctt aat ccg atc gtg gat gct gtc cgc caa tca gat att 449  
53 Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg Gln Ser Asp Ile  
54 30 35 40  
56 gag tgg gtg cac gtt cga aat gag gaa gcg gcg gcg ttt gca gcc ggt 497  
57 Glu Trp Val His Val Arg Asn Glu Glu Ala Ala Ala Phe Ala Ala Gly  
58 45 50 55  
60 gcg gaa tcg ttg atc act ggg gag ctg gca gta tgt gct gct tct tgt 545  
61 Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys Ala Ala Ser Cys  
62 60 65 70  
64 ggt cct gga aac aca cac ctg att cag ggt ctt tat gat tcg cat cga 593  
65 Gly Pro Gly Asn Thr His Leu Ile Gln Gly Leu Tyr Asp Ser His Arg  
66 75 80 85  
68 aat ggt gcg aag gtg ttg gcc atc gct agc cat att ccg agt gcc cag 641  
69 Asn Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile Pro Ser Ala Gln  
70 90 95 100 105

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72 att ggt tgc acg ttc ttc cag gaa acg cat ccg gag att ttg ttt aag 689
73 Ile Gly Ser Thr Phe Phe Gln Glu Thr His Pro Glu Ile Leu Phe Lys
74 110 115 120
76 gaa tgc tct ggt tac tgc gag atg gtg aat ggt ggt gag cag ggt gaa 737
77 Glu Cys Ser Gly Tyr Cys Glu Met Val Asn Gly Gly Glu Gln Gly Glu
78 125 130 135
80 cgc att ttg cat cac gcg att cag tcc acc atg gcg ggt aaa ggt gtg 785
81 Arg Ile Leu His His Ala Ile Gln Ser Thr Met Ala Gly Lys Gly Val
82 140 145 150
84 tgc gtg gta gtg att cct ggt gat atc gct aag gaa gac gca ggt gac 833
85 Ser Val Val Val Ile Pro Gly Asp Ile Ala Lys Glu Asp Ala Gly Asp
86 155 160 165
88 ggt act tat tcc aat tcc act att tct tct ggc act cct gtg gtg ttc 881
89 Gly Thr Tyr Ser Asn Ser Thr Ile Ser Ser Gly Thr Pro Val Val Phe
90 170 175 180 185
92 ccg gat cct act gag gct gca gcg ctg gtg gag gcg att aac aac gct 929
93 Pro Asp Pro Thr Glu Ala Ala Ala Leu Val Glu Ala Ile Asn Asn Ala
94 190 195 200
96 aag tct gtc act ttg ttc tgc ggt gcg ggc gtg aag aat gct cgc gcg 977
97 Lys Ser Val Thr Leu Phe Cys Gly Ala Gly Val Lys Asn Ala Arg Ala
98 205 210 215
100 cag gtg ttg gag ttg gcg gag aag att aaa tca ccg atc ggg cat gcg 1025
101 Gln Val Leu Glu Leu Ala Glu Lys Ile Lys Ser Pro Ile Gly His Ala
102 220 225 230
104 ctg ggt ggt aag cag tac atc cag cat gag aat ccg ttt gag gtc ggc 1073
105 Leu Gly Gly Lys Gln Tyr Ile Gln His Glu Asn Pro Phe Glu Val Gly
106 235 240 245
108 atg tct ggc ctg ctt ggt tac ggc gcc tgc gtg gat gcg tcc aat gag 1121
109 Met Ser Gly Leu Leu Gly Tyr Gly Ala Cys Val Asp Ala Ser Asn Glu
110 250 255 260 265
112 gcg gat ctg ctg att cta ttg ggt acg gat ttc cct tat tct gat ttc 1169
113 Ala Asp Leu Leu Ile Leu Leu Gly Thr Asp Phe Pro Tyr Ser Asp Phe
114 270 275 280
116 ctt cct aaa gac aac gtt gcc cag gtg gat atc aac ggt gcg cac att 1217
117 Leu Pro Lys Asp Asn Val Ala Gln Val Asp Ile Asn Gly Ala His Ile
118 285 290 295
120 ggt cga cgt acc acg gtg aag tat ccg gtg acc ggt gat gtt gct gca 1265
121 Gly Arg Arg Thr Thr Val Lys Tyr Pro Val Thr Gly Asp Val Ala Ala
122 300 305 310
124 aca atc gaa aat att ttg cct cat gtg aag gaa aaa aca gat cgt tcc 1313
125 Thr Ile Glu Asn Ile Leu Pro His Val Lys Glu Lys Thr Asp Arg Ser
126 315 320 325
128 ttc ctt gat cgg atg ctc aag gca cac gag cgt aag ttg agc tgc gtg 1361
129 Phe Leu Asp Arg Met Leu Lys Ala His Glu Arg Lys Leu Ser Ser Val
130 330 335 340 345
132 gta gag acg tac aca cat aac gtc gag aag cat gtg cct att cac cct 1409
133 Val Glu Thr Tyr Thr His Asn Val Glu Lys His Val Pro Ile His Pro
134 350 355 360
136 gaa tac gtt gcc tct att ttg aac gag ctg gcg gat aag gat gcg gtg 1457

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137 Glu Tyr Val Ala Ser Ile Leu Asn Glu Leu Ala Asp Lys Asp Ala Val
138          365          370          375
140 ttt act gtg gat acc ggc atg tgc aat gtg tgg cat gcg agg tac atc 1505
141 Phe Thr Val Asp Thr Gly Met Cys Asn Val Trp His Ala Arg Tyr Ile
142          380          385          390
144 gag aat ccg gag gga acg cgc gac ttt gtg ggt tca ttc cgc cac ggc 1553
145 Glu Asn Pro Glu Gly Thr Arg Asp Phe Val Gly Ser Phe Arg His Gly
146          395          400          405
148 acg atg gct aat gcg ttg cct cat gcg att ggt gcg caa agt gtt gat 1601
149 Thr Met Ala Asn Ala Leu Pro His Ala Ile Gly Ala Gln Ser Val Asp
150 410          415          420          425
152 cga aac cgc cag gtg atc gcg atg tgt ggc gat ggt ggt ttg ggc atg 1649
153 Arg Asn Arg Gln Val Ile Ala Met Cys Gly Asp Gly Gly Leu Gly Met
154          430          435          440
156 ctg ctg ggt gag ctt ctg acc gtt aag ctg cac caa ctt ccg ctg aag 1697
157 Leu Leu Gly Glu Leu Leu Thr Val Lys Leu His Gln Leu Pro Leu Lys
158          445          450          455
160 gct gtg gtg ttt aac aac agt tct ttg ggc atg gtg aag ttg gag atg 1745
161 Ala Val Val Phe Asn Asn Ser Ser Leu Gly Met Val Lys Leu Glu Met
162          460          465          470
164 ctc gtg gag gga cag cca gaa ttt ggt act gac cat gag gaa gtg aat 1793
165 Leu Val Glu Gly Gln Pro Glu Phe Gly Thr Asp His Glu Glu Val Asn
166          475          480          485
168 ttc gca gag att gcg gcg gct gcg ggt atc aaa tcg gta cgc atc acc 1841
169 Phe Ala Glu Ile Ala Ala Ala Ala Gly Ile Lys Ser Val Arg Ile Thr
170 490          495          500          505
172 gat ccg aag aaa gtt cgc gag cag cta gct gag gca ttg gca tat cct 1889
173 Asp Pro Lys Lys Val Arg Glu Gln Leu Ala Glu Ala Leu Ala Tyr Pro
174          510          515          520
177 gga cct gta ctg atc gat atc gtc acg gat cct aat gcg ctg tcg atc 1937
178 Gly Pro Val Leu Ile Asp Ile Val Thr Asp Pro Asn Ala Leu Ser Ile
179          525          530          535
181 cca cca acc atc acg tgg gaa cag gtc atg gga ttc agc aag gcg gcc 1985
182 Pro Pro Thr Ile Thr Trp Glu Gln Val Met Gly Phe Ser Lys Ala Ala
183          540          545          550
185 acc cga acc gtc ttt ggt gga gga gta gga gcg atg atc gat ctg gcc 2033
186 Thr Arg Thr Val Phe Gly Gly Gly Val Gly Ala Met Ile Asp Leu Ala
187          555          560          565
189 cgt tcg aac ata agg aat att cct act cca tgatgattga tacacctgct 2083
190 Arg Ser Asn Ile Arg Asn Ile Pro Thr Pro
191 570          575
193 gttctcattg accgcgagcg cttaactgcc aacatttcca ggatggcagc tcacgcggt 2143
195 gcccatgaga ttgccct 2160
198 <210> SEQ ID NO: 2
199 <211> LENGTH: 579
200 <212> TYPE: PRT
201 <213> ORGANISM: Corynebacterium glutamicum
203 <400> SEQUENCE: 2
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280 Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro  
 281                      405                      410                      415  
 283 His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala  
 284                      420                      425                      430  
 286 Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr  
 287                      435                      440                      445  
 289 Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser  
 290                      450                      455                      460  
 292 Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu  
 293 465                      470                      475                      480  
 295 Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala  
 296                      485                      490                      495  
 298 Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu  
 299                      500                      505                      510  
 301 Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile  
 302                      515                      520                      525  
 304 Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu  
 305                      530                      535                      540  
 307 Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly  
 308 545                      550                      555                      560  
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318 <210> SEQ ID NO: 3

319 <211> LENGTH: 875

320 <212> TYPE: DNA

321 <213> ORGANISM: Corynebacterium glutamicum

323 <400> SEQUENCE: 3

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 326 gcaggtgacg gtacttattc caattccact atttcttctg gcaactcctg ggtgttccc 180  
 327 gatcctactg aggctgcagc gctggtggag gcgattaaca acgctaagtc tgtcactttg 240  
 328 ttctgcggtg cgggcgtgaa gaatgctcgc gcgcagggtg tggagttggc ggagaagatt 300  
 329 aaatcaccga tcgggcatgc gctgggtggg aagcagtaca tccagcatga gaatccgttt 360  
 330 gaggtcggca tgtctggcct gcttggttac ggcgctgcg tggatgcgtc caatgaggcg 420  
 331 gatctgctga ttctattggg tacggatttc ccttattctg atttcccttc taaagacaac 480  
 332 gttgcccagg tggatatcaa cggtgcgcac attggtcgac gtaccacggt gaagtatccg 540  
 333 gtgaccggtg atgttgctgc aacaatcgaa aatattttgc ctcatgtgaa ggaaaaaaca 600  
 334 gatcgttctt tccttgatcg gatgctcaag gcacacgagc gtaagttgag ctcggtggta 660  
 335 gagacgtaca cacataacgt cgagaagcat gtgcctattc accctgaata cgttgcctct 720  
 336 attttgaacg agctggcgga taaggatgcg gtgtttactg tggataccgg catgtgcaat 780  
 337 gtgtggcatg cgaggtaaat cgagaatccg gagggaaacg gcgactttgt gggttcattc 840  
 338 cgccacggca cgatggctaa tgcgttgect catgc 875

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VERIFICATION SUMMARY

DATE: 02/26/2001

PATENT APPLICATION: US/09/456,306

TIME: 10:32:19

Input Set : A:\ES.txt

Output Set: N:\CRF3\02262001\I456306.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

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